

Proc Natl Acad Sci U S A. 2013 Apr 2;110(14):E1254-62. doi: 10.1073/pnas.1222458110. Epub 2013 Mar 4.

Chaperone activation by unfolding.

Foit L, George JS, Zhang BW, Brooks CL 3rd, Bardwell JC.

Source

Howard Hughes Medical Institute and Department of Chemistry and Biophysics Program, University of Michigan, Ann Arbor, MI 48109-1055.

Abstract

Conditionally disordered proteins can alternate between highly ordered and less ordered configurations under physiological conditions. Whereas protein function is often associated with the ordered conformation, for some of these conditionally unstructured proteins, the opposite applies: Their activation is associated with their unfolding. An example is the small periplasmic chaperone HdeA, which is critical for the ability of enteric bacterial pathogens like *Escherichia coli* to survive passage through extremely acidic environments, such as the human stomach. At neutral pH, HdeA is a chaperone-inactive dimer. On a shift to low pH, however, HdeA monomerizes, partially unfolds, and becomes rapidly active in preventing the aggregation of substrate proteins. By mutating two aspartic acid residues predicted to be responsible for the pH-dependent monomerization of HdeA, we have succeeded in isolating an HdeA mutant that is active at neutral pH. We find this HdeA mutant to be substantially destabilized, partially unfolded, and mainly monomeric at near-neutral pH at a concentration at which it prevents aggregation of a substrate protein. These results provide convincing evidence for direct activation of a protein by partial unfolding.

Proc Natl Acad Sci U S A. 2013 Apr 2;110(14):5428-33. doi: 10.1073/pnas.1303279110. Epub 2013 Mar 18.

Molecular chaperone Hsp110 rescues a vesicle transport defect produced by an ALS-associated mutant SOD1 protein in squid axoplasm.

Song Y, Nagy M, Ni W, Tyagi NK, Fenton WA, López-Giráldez F, Overton JD, Horwich AL,

Brady ST.

Source

Department of Neurology, and F.M. Kirby Department of Neurobiology, Boston Children's Hospital, Harvard Medical School, Boston, MA 02115.

Abstract

Mutant human Cu/Zn superoxide dismutase 1 (SOD1) is associated with motor neuron toxicity and death in an inherited form of amyotrophic lateral sclerosis (ALS; Lou Gehrig disease). One aspect of toxicity in motor neurons involves diminished fast axonal transport, observed both in transgenic mice and, more recently, in axoplasm isolated from squid giant axons. The latter effect appears to be directly mediated by misfolded SOD1, whose addition activates phosphorylation of p38 MAPK and phosphorylation of kinesin. Here, we observe that several different oligomeric states of a fusion protein, comprising ALS-associated human G85R SOD1 joined with yellow fluorescent protein (G85R SOD1YFP), which produces ALS in transgenic mice, inhibited anterograde transport when added to squid axoplasm. Inhibition was blocked both by an apoptosis signal-regulating kinase 1 (ASK1; MAPKKK) inhibitor and by a p38 inhibitor, indicating the transport defect is mediated through the MAPK cascade. In further incubations, we observed that addition of the mammalian molecular chaperone Hsc70, abundantly associated with G85R SOD1YFP in spinal cord of transgenic mice, exerted partial correction of the transport defect, associated with diminished phosphorylation of p38. Most striking, the addition of the molecular chaperone Hsp110, in a concentration substoichiometric to the mutant SOD1 protein, completely rescued both the transport defect and the phosphorylation of p38. Hsp110 has been demonstrated to act as a nucleotide exchange factor for Hsc70 and, more recently, to be able to cooperate with it to mediate protein disaggregation. We speculate that it can cooperate with endogenous squid Hsp(c)70 to mediate binding and/or disaggregation of mutant SOD1 protein, abrogating toxicity.

1. Science. 2013 Mar 29;339(6127):1586-9. doi: 10.1126/science.1230758. Epub 2013 Feb 7.

Ultrafast tryptophan-to-heme electron transfer in myoglobins revealed by UV 2D spectroscopy.

Consani C, Auböck G, van Mourik F, Chergui M.

Laboratory of Ultrafast Spectroscopy, École Polytechnique Fédérale de Lausanne, Lausanne, Switzerland.

Comment in

Science. 2013 Mar 29;339(6127):1530-1.

Tryptophan is commonly used to study protein structure and dynamics, such as protein folding, as a donor in fluorescence resonant energy transfer (FRET) studies. By using ultra-broadband ultrafast two-dimensional (2D) spectroscopy in the ultraviolet (UV) and transient absorption in the visible range, we have disentangled the excited state decay pathways of the tryptophan amino acid residues in ferric myoglobins (MbCN and metMb). Whereas the more distant tryptophan (Trp(7)) relaxes by energy transfer to the heme, Trp(14) excitation predominantly decays by electron transfer to the heme. The excited Trp(14)→heme electron transfer occurs in <40 picoseconds with a quantum yield of more than 60%, over an edge-to-edge distance below ~10 angstroms, outcompeting the FRET process. Our results raise the question of whether such electron transfer pathways occur in a larger class of proteins.

PMID: 23393092 [PubMed - indexed for MEDLINE]

2. Science. 2013 Mar 29;339(6127):1608-11. doi: 10.1126/science.1230200. Epub 2013 Feb 28.

Wild pollinators enhance fruit set of crops regardless of honey bee abundance.

Garibaldi LA, Steffan-Dewenter I, Winfree R, Aizen MA, Bommarco R, Cunningham SA, Kremen C, Carvalheiro LG, Harder LD, Afik O, Bartomeus I, Benjamin F, Boreux V, Cariveau D, Chacoff NP, Dudenhöffer JH, Freitas BM, Ghazoul J, Greenleaf S, Hipólito J, Holzschuh A, Howlett B, Isaacs R, Javorek SK, Kennedy CM, Krewenka KM, Krishnan S, Mandelik Y, Mayfield MM, Motzke I, Munyuli T, Nault BA, Otieno M, Petersen J, Pisanty G, Potts SG, Rader R, Ricketts TH, Rundlöf M, Seymour CL, Schüepp C, Szentgyörgyi H, Taki H, Tschardt T, Vergara CH, Viana BF, Wanger TC, Westphal C, Williams N, Klein AM.

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Comment in

Science. 2013 Mar 29;339(6127):1532-3.

The diversity and abundance of wild insect pollinators have declined in many agricultural landscapes. Whether such declines reduce crop yields, or are mitigated by managed pollinators such as honey bees, is unclear. We found universally positive associations of fruit set with flower visitation by wild insects in 41 crop systems worldwide. In contrast, fruit set increased significantly with flower visitation by honey bees in only 14% of the systems surveyed. Overall, wild insects pollinated crops more effectively; an increase in wild insect visitation enhanced fruit set by twice as much as an equivalent increase in honey bee visitation. Visitation by wild insects and honey bees promoted fruit set independently, so pollination by managed honey bees supplemented, rather than substituted for, pollination by wild insects. Our results suggest that new practices for integrated management of both honey bees and diverse wild insect assemblages will enhance global crop yields.

PMID: 23449997 [PubMed - indexed for MEDLINE]

3. Science. 2013 Mar 29;339(6127):1611-5. doi: 10.1126/science.1232728. Epub 2013 Feb 28.

Plant-pollinator interactions over 120 years: loss of species, co-occurrence, and function.

Burkle LA, Marlin JC, Knight TM.

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Comment in

Science. 2013 Mar 29;339(6127):1532-3.

Using historic data sets, we quantified the degree to which global change over 120 years disrupted plant-pollinator interactions in a temperate forest understory community in Illinois, USA. We found degradation of interaction network structure and function and extirpation of 50% of bee species. Network changes can be attributed to shifts in forb and bee phenologies resulting in temporal mismatches, nonrandom species extinctions, and loss of spatial co-occurrences between extant species in modified landscapes. Quantity and quality of pollination services have declined through time. The historic network

showed flexibility in response to disturbance; however, our data suggest that networks will be less resilient to future changes.

PMID: 23449999 [PubMed - indexed for MEDLINE]

4. FEBS Lett. 2013 Apr 17;587(8):1008-11. doi: 10.1016/j.febslet.2012.12.023. Epub 2013 Jan 11.

Protein dynamics in living cells studied by in-cell NMR spectroscopy.

Li C, Liu M.

Key Laboratory of Magnetic Resonance in Biological Systems, State Key Laboratory of Magnetic Resonance and Molecular and Atomic Physics, Wuhan Center for Magnetic Resonance, Wuhan Institute of Physics and Mathematics, Chinese Academy of Sciences, Wuhan 430072, PR China. Electronic address: conggangli@wipm.ac.cn.

Most proteins function in cells where protein concentrations can reach 400g/l. However, most quantitative studies of protein properties are performed in idealized, dilute conditions. Recently developed in-cell NMR techniques can provide protein structure and other biophysical properties inside living cells at atomic resolution. Here we review how protein dynamics, including global and internal motions have been characterized by in-cell NMR, and then discuss the remaining challenges and future directions.

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PMID: 23318712 [PubMed - in process]

5. FEBS Lett. 2013 Apr 17;587(8):1012-20. doi: 10.1016/j.febslet.2013.01.005. Epub 2013 Jan 18.

Native mass spectrometry of photosynthetic pigment-protein complexes.

Zhang H, Cui W, Gross ML, Blankenship RE.

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Native mass spectrometry (MS), or as is sometimes called "native electrospray ionization" allows proteins in their native or near-native states in solution to be introduced into the gas phase and interrogated by mass spectrometry. This approach is now a powerful tool to investigate protein complexes. This article reviews the background of native MS of protein complexes and describes its strengths, taking photosynthetic pigment-protein complexes as examples. Native MS can be utilized in combination with other MS-based approaches to obtain complementary information to that provided by tools such as X-ray crystallography and NMR spectroscopy to understand the structure-function relationships of protein complexes. When additional information beyond that provided by native MS is required, other MS-based strategies can be successfully applied to augment the results of native MS.

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PMID: 23337874 [PubMed - in process]

Nature of Structural and Molecular Biology (April – Current issue)

Characterization of prion-like conformational changes of the neuronal isoform of *Aplysia* CPEB

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Columbia University, New York, USA.

The neuronal isoform of cytoplasmic polyadenylation element-binding protein (CPEB) is a regulator of local protein synthesis at synapses and is critical in maintaining learning-related synaptic plasticity in *Aplysia*. Previous studies indicate that the function of *Aplysia* CPEB can be modulated by conversion to a stable prion-like state, thus contributing to the stabilization of long-term memory on a molecular level. Here, we used biophysical methods to demonstrate that *Aplysia* CPEB, like other prions, undergoes a conformational switch from soluble α -helix-rich oligomer to β -sheet-rich fiber *in vitro*. Solid-state NMR analyses of the fibers indicated a relatively rigid N-terminal prion domain. The fiber form of *Aplysia* CPEB showed enhanced binding to target mRNAs as compared to the soluble form. Consequently, we propose a model for the *Aplysia* CPEB fibers that may have relevance for functional prions in general. Although significant knowledge of cellular and molecular mechanisms underlying the acquisition and early storage of implicit and explicit long-term memory has been gained, the mechanisms by which memories are maintained for long periods of time are still not fully understood. Because proteins normally have relatively short half-lives, of hours or days, the question remains: How can the change in molecular

composition of a synapse be maintained for long periods of time, as is required for long-term memory? We previously found one answer to this conundrum in a work describing a prion-like regulator of local protein synthesis at the synapse in the marine snail *Aplysia californica*: the cytoplasmic polyadenylation element-binding protein *Aplysia* CPEB. This provided physiological evidence that the prion-like properties of *Aplysia* CPEB might explain the self-sustained, continuous molecular turnover at the synapse.

Detecting endogenous SUMO targets in mammalian cells and tissues

Janina Becker, Sina V Barysch, Samir Karaca, Claudia Dittner, He-Hsuan Hsiao, Mauricio Berriel Diaz, Stephan Herzig, Henning Urlaub & Frauke Melchior

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SUMOylation is an essential modification that regulates hundreds of proteins in eukaryotic cells. Owing to its dynamic nature and low steady-state levels, endogenous SUMOylation is challenging to detect. Here, we present a method that allows efficient enrichment and identification of endogenous targets of SUMO1 and the nearly identical SUMO2 and 3 (SUMO 2/3) from vertebrate cells and complex organ tissue. Using monoclonal antibodies for which we mapped the epitope, we enriched SUMOylated proteins by immunoprecipitation and peptide elution. We used this approach in combination with MS to identify SUMOylated proteins, which resulted in the first direct comparison of the endogenous SUMO1- and SUMO2/3-modified proteome in mammalian cells, to our knowledge. This protocol provides an affordable and feasible tool to investigate endogenous SUMOylation in primary cells, tissues and organs, and it will facilitate understanding of SUMO's role in physiology and disease.

Interplay between Heat Shock Proteins HSP101 and HSA32 Prolongs Heat Acclimation Memory Posttranscriptionally in *Arabidopsis*¹[W][OA]

Ting-ying Wu², Yu-ting Juan², Yang-hsin Hsu, Sze-hsien Wu, Hsiu-ting Liao, Raymond W.M. Fung, and Yee-yung Charng*

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Heat acclimation improves the tolerance of organisms to severe heat stress. Our previous work showed that in *Arabidopsis* (*Arabidopsis thaliana*), the “memory” of heat acclimation treatment decayed faster in the absence of the heat-stress-associated 32-kD protein HSA32, a heat-induced protein predominantly found in plants. The HSA32 null mutant attains normal short-term-acquired thermotolerance but is defective in long-term acquired thermotolerance. To further explore this phenomenon, we isolated *Arabidopsis* defective in

long-term acquired thermotolerance (dlt) mutants using a forward genetic screen. Two recessive missense alleles, *dlt1-1* and *dlt1-2*, encode the molecular chaperone heat shock protein101 (HSP101). Results of immunoblot analyses suggest that HSP101 enhances the translation of HSA32 during recovery after heat treatment, and in turn, HSA32 retards the decay of HSP101. The *dlt1-1* mutation has little effect on HSP101 chaperone activity and thermotolerance function but compromises the regulation of HSA32. In contrast, *dlt1-2* impairs the chaperone activity and thermotolerance function of HSP101 but not the regulation of HSA32. These results suggest that HSP101 has a dual function, which could be decoupled by the mutations. Pulse-chase analysis showed that HSP101 degraded faster in the absence of HSA32. The autophagic proteolysis inhibitor E-64d, but not the proteasome inhibitor MG132, inhibited the degradation of HSP101. Ectopic expression of HSA32 confirmed its effect on the decay of HSP101 at the posttranscriptional level and showed that HSA32 was not sufficient to confer long-term acquired thermotolerance when the HSP101 level was low. Taken together, we propose that a positive feedback loop between HSP101 and HSA32 at the protein level is a novel mechanism for prolonging the memory of heat acclimation.

Transcriptome Responses to Combinations of Stresses in *Arabidopsis*¹[W][OA]

Simon Rasmussen, Pankaj Barah, Maria Cristina Suarez-Rodriguez², Simon Bressendorff, Pia Friis³, Paolo Costantino, Atle M. Bones, Henrik Bjørn Nielsen, and John Mundy*

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Biotic and abiotic stresses limit agricultural yields, and plants are often simultaneously exposed to multiple stresses. Combinations of stresses such as heat and drought or cold and high light intensity have profound effects on crop performance and yields. Thus, delineation of the regulatory networks and metabolic pathways responding to single and multiple concurrent stresses is required for breeding and engineering crop stress tolerance. Many studies have described transcriptome changes in response to single stresses. However, exposure of plants to a combination of stress factors may require agonistic or antagonistic responses or responses potentially unrelated to responses to the corresponding single stresses. To analyze such responses, we initially compared transcriptome changes in 10 *Arabidopsis* (*Arabidopsis thaliana*) ecotypes using cold, heat, high-light, salt, and flagellin treatments as single stress factors as well as their double combinations. This revealed that some 61% of the transcriptome changes in response to double stresses were not predictable from the responses to single stress treatments. It also showed that plants prioritized between potentially antagonistic responses for only 5% to 10% of the responding transcripts. This indicates that plants have evolved to cope with combinations of stresses and, therefore, may be bred to endure them. In addition, using a subset of this data from

the Columbia and Landsberg erecta ecotypes, we have delineated coexpression network modules responding to single and combined stresses.

Disease Resistance Gene-Induced Growth Inhibition Is Enhanced by *rcd1* Independent of Defense Activation in *Arabidopsis*

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State Key Laboratory Breeding Base for Zhejiang Sustainable Pest and Disease Control, Institute of Virology and Biotechnology, Zhejiang Academy of Agricultural Sciences, Hangzhou 310021, China (Y.Z.); Department of Plant Biology, Cornell University, Ithaca, New York 14853 (Y.Z., B.D., J.Q., B.Z., J.H.); Sichuan Agricultural University, Chengdu 611130, China (B.D.); and Nanjing Agricultural University, Nanjing 210095, China (B.Z.)

Activation of plant immune responses is often associated with an inhibition of plant growth. The molecular mechanisms underlying this fitness cost are unknown. Here, we utilize the autoimmune response mutant suppressor of *npr1*, *constitutive1* (*snc1*) resulting from an activated form of the Disease Resistance (R) gene to dissect the genetic component mediating growth inhibition in *Arabidopsis* (*Arabidopsis thaliana*). The radical-induced cell death1 (*rcd1*) mutant defective in responses to reactive oxygen species (ROS) was isolated as an enhancer of the *snc1* mutant in growth inhibition but not in defense response activation. Similarly, the vitamin C2 (*vtc2*) and *vtc3* mutants defective in ROS detoxification enhanced the growth defects of *snc1*. Thus, perturbation of ROS status by R gene activation is responsible for the growth inhibition, and this effect is independent of defense response activation. This was further supported by the partial rescue of growth defects of *rcd1 snc1* by the respiratory burst oxidase homolog D (*rbohD*) and *rbohF* mutations compromising the generation of ROS burst. Collectively, these findings indicate that perturbation of ROS homeostasis contributes to the fitness cost independent of defense activation.

Gibert B et al. Knock down of heat shock protein 27 (Hsp B1) induces degradation of several putative client proteins. PLoS ONE 2012;7:e29719.

Journal of Photochemistry and Photobiology B: Biology: Alert 2 April-8 April

[Ultra-weak photon emission as a non-invasive tool for the measurement of oxidative stress induced by UVA radiation in *Arabidopsis thaliana*](#) Original Research Article

Available online 6 April 2013

Anshu Rastogi, Pavel Pospíšil

Current opinion in plant biology
[Promise and issues of genetically modified crops](#) Review Article

Available online 6 April 2013
Hao Chen, Yongjun Lin

Current Opinion in Microbiology: Alert 2 April-8 April

[Microbial amyloids – functions and interactions within the host](#) Review Article

Pages 93-99
Kelly Schwartz, Blaise R Boles

► Numerous examples of functional amyloids are emerging in diverse bacterial species. ► Bacterial functional amyloids facilitate a multitude of interactions with the host. ► Functions of bacterial amyloids include roles in: biofilm development, toxin storage, sporulation, and modulation of the immune response.

Analytical Biochemistry: Alert 1 April-7 April

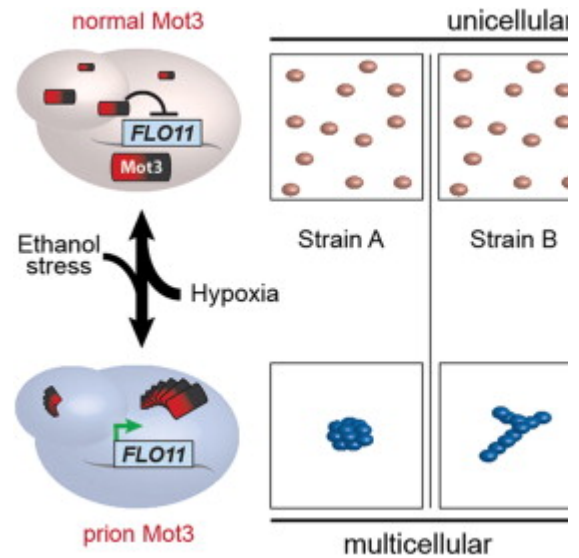
[Highlighting the tricarboxylic acid cycle: Liquid 13C-labeled organic acids](#) Original Research Article

Pages 151-159
Mohamed Koubaa, Jean Christophe Cocuron, Bri

Cell: Alert 1 April-7 April

[Heritable Remodeling of Yeast Multicellularity by an Environmentally Responsive Prion](#) Original Research Article

Pages 153-165
Daniel L. Holmes, Alex K. Lancaster, Susan Lindquist, Randal Halfmann
Graphical Abstract



Highlights

- Prion formation by a yeast transcription factor, Mot3, regulates multicellularity
- Natural environmental changes govern the gain and loss of Mot3 prions
- Mot3 prions interact with genetic variation to diversify multicellular phenotypes

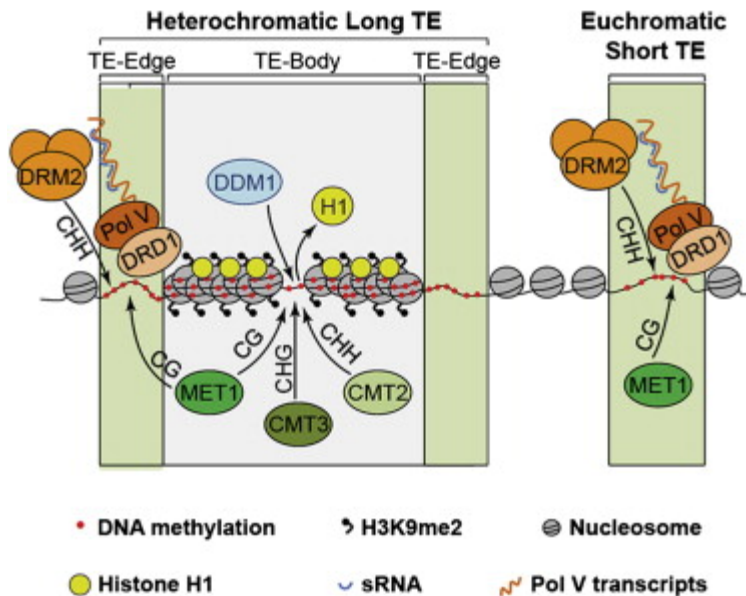
[The *Arabidopsis* Nucleosome Remodeler DDM1 Allows DNA Methyltransferases to Access H1-Containing Heterochromatin](#) Original Research Article

Pages 193-205

Assaf Zemach, M. Yvonne Kim, Ping-Hung Hsieh, Devin Coleman-Derr, Leor Eshed-Williams, Ka Thao, Stacey L. Harmer, Daniel Zilberman

Graphical Abstract

DNA Methylation of Arabidopsis Transposable Elements (TEs)



Highlights

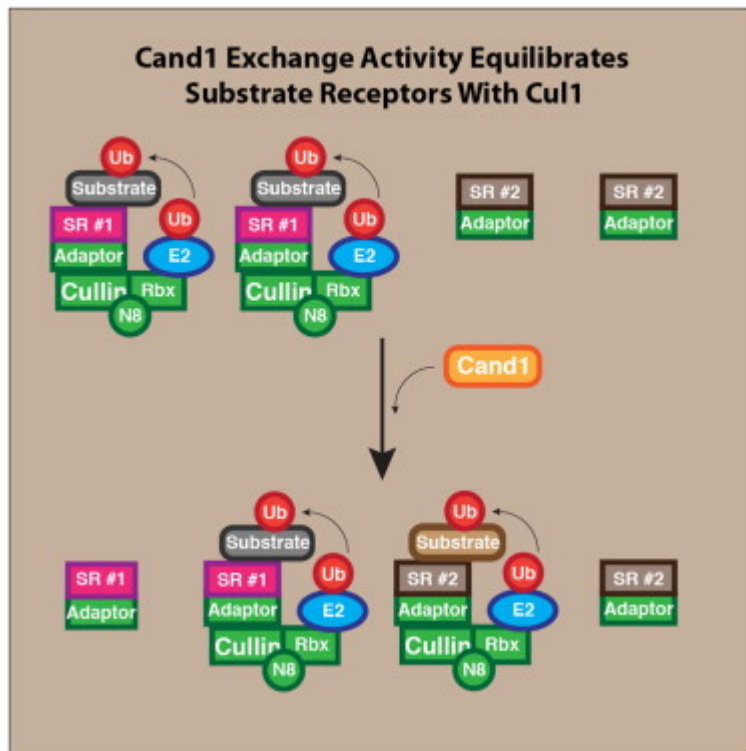
- ▶ DDM1 and RNA-dependent DNA methylation (RdDM) separately regulate DNA methylation
- ▶ Chromatin features determine the requirement for DDM1 and the efficiency of RdDM
- ▶ DDM1 makes heterochromatin bound by H1 accessible to DNA methyltransferases
- ▶ The chromomethylase CMT2 is required for most asymmetric (CHH) methylation

[Cand1 Promotes Assembly of New SCF Complexes through Dynamic Exchange of F Box Proteins](#) Original Research Article

Pages 206-215

Nathan W. Pierce, J. Eugene Lee, Xing Liu, Michael J. Sweredoski, Robert L.J. Graham, Elizabeth A. Larimore, Michael Rome, Ning Zheng, Bruce E. Clurman, Sonja Hess, Shu-ou Shan, Raymond J. Deshaies

Graphical Abstract



Highlights

► Cand1 modulates the repertoire of SCF ubiquitin ligase complexes in cells ► Cand1 functions as an F box protein exchange factor ► FRET assay reveals real-time dynamics of SCFFbxw7 assembly and disassembly ► Cand1 accelerates the dissociation rate of SCFFbxw7 one-million-fold

Mitra A, Basak T, Datta K, Naskar S, Sengupta S, Sarkar S.

Role of α -crystallin B as a regulatory switch in modulating cardiomyocyte apoptosis by mitochondria or endoplasmic reticulum during cardiac hypertrophy and myocardial infarction.

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Chaperonin 60: a paradoxical, evolutionarily conserved protein family with multiple moonlighting functions.

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PMID: 23542375 [PubMed - as supplied by publisher]

Plant, Cell & Environment Content Alert: 36, 5 (May 2013)

Review

Involvement of auxin pathways in modulating root architecture during beneficial plant-microorganism interactions (pages 909-919)

POORNIMA SUKUMAR, VALÉRIE LEGUÉ, ALICE VAYSSIÈRES, FRANCIS MARTIN, GERALD A. TUSKAN and UDAYA C. KALLURI

Article first published online: 11 DEC 2012 | DOI: 10.1111/pce.12036

The community of researchers studying molecular plant-microbe interactions under the banners of fundamental plant science, biofuel-bioenergy, and crop productivity and sustainability research is expanding rapidly. The review summarizes multiple, separate lines of evidences linking auxin transport, signaling, and synthesis pathways to beneficial plant-microbe interactions and modulations in host root architecture. Compelling physiology and functional genomics-based evidence was found in support of a delicate and precise orchestration of distinct root phenotypic effects achieved via a shared auxin biosynthesis and signaling machinery involving signaling crosstalk. A hypothetical and simplified model on role of auxin in beneficial plant-microbe interactions is presented, and outstanding research

challenges and potential future directions are discussed.

[Rhizospheric NO affects N uptake and metabolism in Scots pine \(*Pinus sylvestris* L.\) seedlings depending on soil N availability and N source \(pages 1019–1026\)](#)

JUDY SIMON, FANG DONG, FRANZ BUEGGER and HEINZ RENNENBERG

Article first published online: 3 DEC 2012 | DOI: 10.1111/pce.12034

Signals controlling the competitive interactions for nitrogen between plants and soil microorganisms in the rhizosphere are to date mainly unknown, thus, we investigated the effects of rhizospheric NO concentration with varying soil N availability on N uptake and metabolism in fine roots of Scots pine seedlings. Our results show for the first time that NO affected N uptake by seedlings dependent on N source and soil N availability. The commonly accepted suppression of nitrate uptake in the presence of ammonium and glutamine was overruled at high NO. This study also provides first evidence for the effects of NO on nitrate and arginine uptake in a tree species and that rhizospheric NO does not only affect deciduous trees (*i.e.*, beech), but also coniferous tree species (*i.e.*, pine).

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PMID: 23580434 [PubMed - as supplied by publisher]

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PMID: 23572879 [PubMed]

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J Biol Chem. 2013 Apr 9;. [Epub ahead of print]

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Mutations in TFIIH causing trichothiodystrophy are responsible for defects in ribosomal RNA production and processing.

Hum Mol Genet. 2013 Apr 4;. [Epub ahead of print]

PMID: 23562818 [PubMed - as supplied by publisher]

Cell: Alert 9 April-15 April

[A Mechanism for Localized Lignin Deposition in the Endodermis](#)

Pages 402-412

Yuree Lee, Maria C. Rubio, Julien Alassimone, Niko Geldner

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[Supplementary content](#)

► A specific NADPH oxidase is crucial for formation of lignified Casparian strips ► NADPH oxidase specificity depends on subcellular localization and regulatory domain ► CASPs recruit secreted peroxidases to the Casparian strip domain ► The assembly of NADPH oxidase and peroxidases drives localized lignin formation

CASP scaffolding proteins recruit a specific NADPH oxidase as well as extracellular peroxidases to sites of Casparian strips, diffusion barriers that form via lignin deposition. The combined action of these enzymes regulates ROS levels to drive local lignin polymerization.

Physiologia Plantarum Content Alert (New Articles)

[A lack of mitochondrial alternative oxidase compromises capacity to recover from severe drought stress](#)

Jia Wang and Greg C. Vanlerberghe

Accepted manuscript online: 13 APR 2013 09:57AM EST | DOI: 10.1111/pp1.12059

EMBO J.

Focus issue in 2012:

[Power plants hit the nerve: mitochondria in neurodegeneration](#)

Mitochondria play a central role in many neurodegenerative conditions, among them Alzheimer's, Parkinson's and Huntington's Disease. A series of review articles published in The EMBO Journal illustrates the different ways mitochondrial dysfunction leads to neurodegeneration. Mitochondrial function in neurons can be impaired at the level of biogenesis, respiration, calcium buffering, intramitochondrial and cellular quality control, as well as fission/fusion dynamics and motility.

April 17

[The splicing machinery promotes RNA-directed DNA methylation and transcriptional silencing in Arabidopsis](#)

Components of the splicing machinery are needed for siRNA generation, *de novo* DNA methylation, and transcriptional gene silencing in plants.

Cui-Jun Zhang, Jin-Xing Zhou, Jun Liu, Ze-Yang Ma, Su-Wei Zhang, Kun Dou, Huan-Wei Huang, Tao Cai, Renyi Liu, Jian-Kang Zhu and Xin-Jian He

The EMBO Journal (2013), 32, - 1128 - 1140, doi:10.1038/emboj.2013.49

- [Abstract -](#)
- [Full text](#)
- [PDF \(918 KB\)](#)

TOR and S6K1 promote translation reinitiation of uORF-containing mRNAs via phosphorylation of eIF3h

The phytohormone Auxin activates the TOR pathway to dissociate inactive S6K1 from polysomes and to stimulate phosphorylation of the translation initiation factor eIF3h, resulting in the enhanced translation of uORF-containing mRNAs.

Mikhail Schepetilnikov, Maria Dimitrova, Eder Mancera-Martínez, Angèle Geldreich, Mario Keller and Lyubov A Ryabova

The EMBO Journal (2013), 32, - 1087 - 1102, doi:10.1038/emboj.2013.61

- [Abstract -](#)
- [Full text](#)
- [PDF \(3,316 KB\)](#)

Apr 3

Structural features within the nascent chain regulate alternative targeting of secretory proteins to mitochondria

ER signal peptides can mediate both ER and mitochondrial targeting, depending on structural features in the nascent chain. While proteins containing structured domains are imported into the ER, unstructured polypeptides are targeted to mitochondria.

Natalie V Pfeiffer, Daniela Dirndorfer, Sven Lang, Ulrike K Resenberger, Lisa M Restelli, Charles Hemion, Margit Miesbauer, Stephan Frank, Albert Neutzner, Richard Zimmermann, Konstanze F Winklhofer and Jörg Tatzelt

The EMBO Journal (2013), 32, - 1036 - 1051, doi:10.1038/emboj.2013.46

- [Abstract - Structural features within the nascent chain regulate alternative targeting of secretory proteins to mitochondria](#)
- [Full text](#)
- [PDF \(2,385 KB\)](#)

March 20

Ubc9 acetylation: a new route for achieving specificity in substrate SUMOylation FREE

Post-translational modifications are the key for generating diversity and specificity in a pathway that relies on a minimum number of components.

Shen-Hsi Yang and Andrew D Sharrocks

The EMBO Journal (2013), 32, - 773 - 774, doi:10.1038/emboj.2013.21

- [First paragraph - Ubc9 acetylation: a new route for achieving specificity in substrate SUMOylation](#)
- [Full text](#)
- [PDF \(133 KB\)](#)

Ubc9 acetylation modulates distinct SUMO target modification and hypoxia response

SIRT1-mediated deacetylation modulates the SUMO conjugase Ubc9 to selectively control sumoylation of substrates with an extended consensus motif.

Yung-Lin Hsieh, Hong-Yi Kuo, Che-Chang Chang, Mandar T Naik, Pei-Hsin Liao, Chun-Chen Ho, Tien-Chi Huang, Jen-Chong Jeng, Pang-Hung Hsu, Ming-Daw Tsai, Tai-Huang Huang and Hsiu-Ming Shih

The EMBO Journal (2013), 32, - 791 - 804, doi:10.1038/emboj.2013.5

- [Abstract - Ubc9 acetylation modulates distinct SUMO target modification and hypoxia response](#)
- [Full text](#)
- [PDF \(3,083 KB\)](#)

Feb 20

Running a little late: chloroplast Fe status and the circadian clock FREE

Iron homeostasis is essential for plant growth and survival. Two papers now report that chloroplast Iron levels also regulate the period of the circadian clock, which might confer fitness advantage by linking iron status to daily changes in environmental conditions.

Grandon T Wilson and Erin L Connolly

The EMBO Journal (2013), 32, - 490 - 492, doi:10.1038/emboj.2013.14

- [First paragraph - Running a little late: chloroplast Fe status and the circadian clock](#)
- [Full text](#)

- [PDF \(304 KB\)](#)

Circadian clock adjustment to plant iron status depends on chloroplast and phytochrome function EMBO Open

The circadian clock of *Arabidopsis* is found to be hardwired to cellular iron levels, with chloroplasts playing a central role in iron sensing.

Patrice A Salomé, Michele Oliva, Detlef Weigel and Ute Krämer

The EMBO Journal (2013), 32, - 511 - 523, doi:10.1038/emboj.2012.330

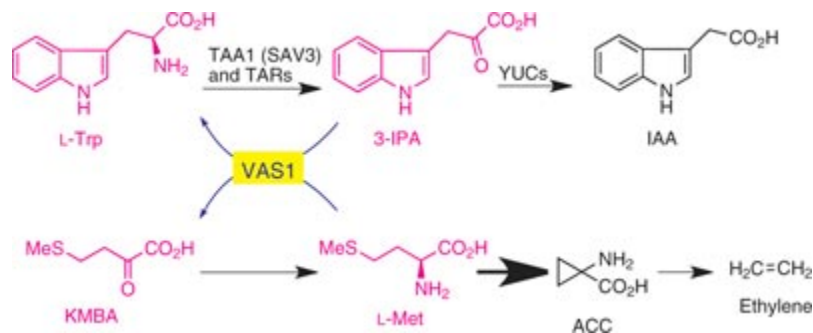
- [Abstract - Circadian clock adjustment to plant iron status depends on chloroplast and phytochrome function](#)
- [Full text](#)
- [PDF \(2,182 KB\)](#)

Nature Chemical Biology

Coordination of auxin and ethylene biosynthesis by the aminotransferase VAS1 - pp244 - 246

Zuyu Zheng, Yongxia Guo, Ondřej Novák, Xinhua Dai, Yunde Zhao, Karin Ljung, Joseph P Noel & Joanne Chory

doi:10.1038/nchembio.1178



The VAS1 aminotransferase regulates the shade avoidance response in *Arabidopsis thaliana* by shunting metabolic flux away from auxin and ethylene, two growth regulatory plant hormones.

[Abstract - Coordination of auxin and ethylene biosynthesis by the aminotransferase VAS1](#) | [Full Text - Coordination of auxin and ethylene biosynthesis by the aminotransferase VAS1](#) | [PDF \(642 KB\) - Coordination of auxin and ethylene biosynthesis by the aminotransferase VAS1](#)

Heat stress induction of *miR398* triggers a regulatory loop that is critical for thermotolerance in *Arabidopsis*

Qingmei Guan, Xiaoyan Lu, Haitao Zeng, Yanyan Zhang and Jianhua Zhu

Accepted manuscript online: 8 MAR 2013 04:47PM EST | DOI: 10.1111/tbj.12169

Science 8 February 2013: Vol. 339 no. 6120 pp. 704-707

DOI: 10.1126/science.1230406

Regulation of Flowering by Trehalose-6-Phosphate Signaling in *Arabidopsis thaliana*

[Vanessa Wahl^{1,*}](#), [Jathish Ponnu²](#), [Armin Schlereth¹](#), [Stéphanie Arrivault¹](#), [Tobias Langenecker²](#), [Annika Franke¹](#), [Regina Feil¹](#), [John E. Lunn¹](#), [Mark Stitt¹](#), [Markus Schmid^{2,*}](#)

Nature Chemical Biology

Structural biology: Protein self-assembly intermediates - pp216 - 217

Michele Vendruscolo & Christopher M Dobson

doi:10.1038/nchembio.1210

Proteins can self-assemble into functional states, or they can end up as aberrant and sometimes toxic aggregates. Metastable intermediate states are often detected in these processes, and their structural characterization provides vital information about the balance between functional and pathological behavior in living systems.

Cold denaturation of a protein dimer monitored at atomic resolution

[Mariusz Jaremko](#), [Łukasz Jaremko](#), [Hai-Young Kim](#), [Min-Kyu Cho](#), [Charles D Schwieters](#), [Karin Giller](#), [Stefan Becker](#) & [Markus Zweckstetter](#)

Nature Chemical Biology 9, 264–270 (2013)

Coordination of auxin and ethylene biosynthesis by the aminotransferase VAS1 - pp244 - 246

Zuyu Zheng, Yongxia Guo, Ondřej Novák, Xinhua Dai, Yunde Zhao, Karin Ljung, Joseph P Noel & Joanne Chory

The VAS1 aminotransferase regulates the shade avoidance response in *Arabidopsis thaliana* by shunting metabolic flux away from auxin and ethylene, two growth regulatory plant hormones.

Mapping QTLs for salt tolerance with additive, epistatic and QTL x treatment interaction effects at seedling stage in wheat

Y. Xu, S. Li, L. Li, X. Zhang, H. Xu and D. An

Article first published online: 13 MAR 2013 | DOI: 10.1111/pbr.12048

Bekh-Ochir D, Shimada S, Yamagami A, Kanda S, Ogawa K, Nakazawa M, Matsui M, Sakuta M, Osada H, Asami T, Nakano T.

A novel mitochondrial DnaJ/Hsp40 family protein BIL2 promotes plant growth and resistance against environmental stress in brassinosteroid signaling.

Planta. 2013 Mar 15;. [Epub ahead of print]

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Chaperone activation by unfolding.

Proc Natl Acad Sci U S A. 2013 Mar 4;. [Epub ahead of print]

PMID: 23487787 [PubMed - as supplied by publisher]

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Nitration of Hsp90 induces cell death.

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Blessings in disguise: biological benefits of prion-like mechanisms.

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Heat stress induction of miR398 triggers a regulatory loop that is critical for thermotolerance in Arabidopsis.

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The Role of AAA+ Proteases in Mitochondrial Protein Biogenesis, Homeostasis and Activity Control.

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Translation elongation factor 1B (eEF1B) is an essential host factor for Tobacco mosaic virus infection in plants.

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Review article: Different anti-aggregation and pro-degradative functions of the members of the mammalian sHSP family in neurological disorders

Serena Carra, Paola Rusmini, Valeria Crippa, Elisa Giorgetti, Alessandra Boncoraglio, Riccardo Cristofani, Maximillian Naujock, Melanie Meister, Melania Minoia, Harm H. Kampinga, and Angelo Poletti

Phil. Trans. R. Soc. B May 5, 2013 368 20110409; doi:10.1098/rstb.2011.0409

<http://rstb.royalsocietypublishing.org/content/368/1617/20110409.abstract.html>

Research article: The specificity of the interaction between α B-crystallin and desmin filaments and its impact on filament aggregation and cell viability

Jayne L. Elliott, Ming Der Perng, Alan R. Prescott, Karin A. Jansen, Gijssje H. Koenderink, and Roy A. Quinlan

Phil. Trans. R. Soc. B May 5, 2013 368 20120375; doi:10.1098/rstb.2012.0375 (open access)

<http://rstb.royalsocietypublishing.org/content/368/1617/20120375.abstract.html>

Review article: Peptide aptamers: tools to negatively or positively modulate HSPB1(27) function

Benjamin Gibert, Stéphanie Simon, Valeriya Dimitrova, Chantal Diaz-Latoud, and André-Patrick Arrigo

Phil. Trans. R. Soc. B May 5, 2013 368 20120075; doi:10.1098/rstb.2012.0075

<http://rstb.royalsocietypublishing.org/content/368/1617/20120075.abstract.html>

Research article: C-terminal interactions mediate the quaternary dynamics of α B-crystallin

Gillian R. Hilton, Georg K. A. Hochberg, Arthur Laganowsky, Scott I. McGinnigle, Andrew J. Baldwin, and Justin L. P. Benesch

Phil. Trans. R. Soc. B May 5, 2013 368 20110405; doi:10.1098/rstb.2011.0405 (open access)

<http://rstb.royalsocietypublishing.org/content/368/1617/20110405.abstract.html>

Research article: Changes in the quaternary structure and function of MjHSP16.5 attributable to deletion of the IXI motif and introduction of the substitution, R107G, in the α -crystallin domain

Roy A. Quinlan, Yan Zhang, Andrew Lansbury, Ian Williamson, Ehmke Pohl, and Fei Sun

Phil. Trans. R. Soc. B May 5, 2013 368 20120327; doi:10.1098/rstb.2012.0327 (open access)

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Review article: Assembly chaperones: a perspective

R. John Ellis

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Mechanism of an ATP-independent protein disaggregase. II. Distinct molecular interactions drive multiple steps during aggregate disassembly.

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Surveillance-Activated Defenses Block the ROS-Induced Mitochondrial Unfolded Protein Response.

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Defects in IRE1 enhance cell death and fail to degrade mRNAs encoding secretory pathway proteins in the Arabidopsis unfolded protein response.

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Current Biology: Alert 16 March-22 March

[Development: CLAVATA1 Joins the Club of Root Stem Cell Regulators](#)

Pages R245-R247

Elisabeth L. Williams, Ive De Smet

[A Dof Transcription Factor, SCAP1, Is Essential for the Development of Functional Stomata in Arabidopsis](#)

Pages 479-484

Juntaro Negi, Kosuke Moriwaki, Mineko Konishi, Ryusuke Yokoyama, Toshiaki Nakano, Kensuke Kusumi, Mimi Hashimoto-Sugimoto, Julian I. Schroeder, Kazuhiko Nishitani, Shuichi Yanagisawa, Koh Iba

Highlights

► scap1 is a mutant that impairs functional movement and morphogenesis of stomata ► SCAP1 is a Dof-type plant transcription factor expressed in maturing guard cells ► SCAP1 directly regulates key elements of stomatal functioning

[A Mitochondrial Ribosomal and RNA Decay Pathway Blocks Cell Proliferation](#)

Pages 535-541

Uwe Richter, Taina Lahtinen, Paula Marttinen, Maarit Myöhänen, Dario Greco, Giuseppe Cannino, Howard T. Jacobs, Niina Lietzén, Tuula A. Nyman, Brendan J. Battersby

Highlights

► Pharmacological inhibition of peptide deformylase stalls mitochondrial ribosomes ► Stalled mitochondrial ribosomes trigger a ribosome quality-control pathway ► Activation of mito-ribosome quality-control pathway impairs cell proliferation ► Actinonin leads to the depletion of mito-ribosomes and RNA

Nature Reviews Molecular Cell Biology contents April 2013 Volume 14 Number 4

Diversity in the origins of proteostasis networks — a driver for protein function in evolution

Evan T. Powers & William E. Balch

p237 | doi:10.1038/nrm3542

All three domains of life - Bacteria, Archaea and Eukarya - have a proteostasis network that modulates protein folding in response to changes in the environment and to genetic variation. This proteostasis network has co-evolved with the proteome and is thought to play a part in driving evolution.

[Abstract](#) | [Full Text](#) | [PDF](#) | [Supplementary information](#)

Is Oxidized Thioredoxin a Major Trigger for Cysteine Oxidation? Clues from a Redox Proteomics Approach

Sarela García-Santamarina, Susanna Boronat, Isabel A. Calvo, Miguel Rodríguez-Gabriel, José Ayté, Henrik Molina, and Elena Hidalgo

Antioxidants & Redox Signaling, Vol. 18, No. 13, May 2013: 1549-1556.

[Abstract](#) | [Full Text HTML](#) | [Full Text PDF \(546 KB\)](#) | [Full Text PDF with Links \(344 KB\)](#)

Comprehensive Invited Review

Principles in Redox Signaling: From Chemistry to Functional Significance

Alberto Bindoli and Maria Pia Rigobello

Antioxidants & Redox Signaling, Vol. 18, No. 13, May 2013: 1557-1593.

[Abstract](#) | [Full Text HTML](#) | [Full Text PDF \(1410 KB\)](#) | [Full Text PDF with Links \(1122 KB\)](#)

Thiol–Disulfide Exchange in Signaling: Disulfide Bonds As a Switch

Joris Messens and Jean-François Collet

Antioxidants & Redox Signaling, Vol. 18, No. 13, May 2013: 1594-1596.

[Abstract](#) | [Full Text HTML](#) | [Full Text PDF \(133 KB\)](#) | [Full Text PDF with Links \(97 KB\)](#)

Forum Original Research Communication

Inaccurately Assembled Cytochrome c Oxidase Can Lead to Oxidative Stress-Induced Growth Arrest

Manuela Bode, Sebastian Longen, Bruce Morgan, Valentina Peleh, Tobias P. Dick, Karl Bihlmaier, and Johannes M. Herrmann

Antioxidants & Redox Signaling, Vol. 18, No. 13, May 2013: 1597-1612.

[Abstract](#) | [Full Text HTML](#) | [Full Text PDF \(1101 KB\)](#) | [Full Text PDF with Links \(809 KB\)](#)

Kinetics and Mechanisms of Thiol–Disulfide Exchange Covering Direct Substitution and Thiol Oxidation-Mediated Pathways

Péter Nagy

Antioxidants & Redox Signaling, Vol. 18, No. 13, May 2013: 1623-1641.

[Abstract](#) | [Full Text HTML](#) | [Full Text PDF \(728 KB\)](#) | [Full Text PDF with Links \(480 KB\)](#)

Low-Molecular-Weight Thiols in Thiol–Disulfide Exchange

Koen Van Laer, Chris J. Hamilton, and Joris Messens

Antioxidants & Redox Signaling, Vol. 18, No. 13, May 2013: 1642-1653.

[Abstract](#) | [Full Text HTML](#) | [Full Text PDF \(701 KB\)](#) | [Full Text PDF with Links \(404 KB\)](#)

Glutaredoxins in Thiol/Disulfide Exchange

Christopher Horst Lillig and Carsten Berndt

Antioxidants & Redox Signaling, Vol. 18, No. 13, May 2013: 1654-1665.

[Abstract](#) | [Full Text HTML](#) | [Full Text PDF \(516 KB\)](#) | [Full Text PDF with Links \(377 KB\)](#)

Functions and Cellular Compartmentation of the Thioredoxin and Glutathione Pathways in Yeast

Michel B. Toledano, Agnès Delaunay-Moisan, Caryn E. Outten, and Aeid Igbaria

Antioxidants & Redox Signaling, Vol. 18, No. 13,

May 2013: 1699-1711.

[Abstract](#) | [Full Text HTML](#) | [Full Text PDF \(694 KB\)](#) | [Full Text PDF with Links \(359 KB\)](#)

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Changes in the quaternary structure and function of MjHSP16.5 attributable to deletion of the IXI motif and introduction of the substitution, R107G, in the $\hat{I}\pm$ -crystallin domain.

Philos Trans R Soc Lond B Biol Sci. 2013;368(1617):20120327.

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Self-assembly of protein aggregates in ageing disorders: the lens and cataract model.

Philos Trans R Soc Lond B Biol Sci. 2013;368(1617):20120104.

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Peptide aptamers: tools to negatively or positively modulate HSPB1(27) function.

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Different anti-aggregation and pro-degradative functions of the members of the mammalian sHSP family in neurological disorders.

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Assembly chaperones: a perspective.

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